with a * for representative P3 (based on the known crystal structures of the parent motifs) in panel A,] and the 12 residues of the Ca-binding loop are shaded [in panel B].

Please replace the paragraph beginning at line 29 on page 9 with the following paragraph:

[Figures 7A-B] Figure 7. [A) Representative] The top panel is a representative gel showing the disappearance of type I band (supercoiled pBR322 plasmid) as a function of increasing EuP3 (5-25 μM). This gel shift is not seen with free metal over the same concentration range (right lanes), or with the control peptide, P2. An attenuated shift is observed for free P3. [B) Quantified] The lower panel is a graph showing quantified volumes of type I band (arbitrary volume units) as a function of EuP3 concentration. Data are an average of three gel shift assays.

In the Claims

Please substitute the claim set in the appendix entitled "Clean Version of Pending Claims" for the previously pending claim set. The specific amendments to individual claims are detailed in the following marked-up set of claims.

Please amend the claims as follows:

1. (Amended) An isolated synthetic peptide or polypeptide comprising a domain which specifically binds a nucleic acid sequence and a domain which specifically binds a metal which is [hydrolytic] hydrolytically or redox active, wherein the domain which specifically binds the metal is within the domain which specifically binds the nucleic acid sequence.

2. (Amended) The peptide or polypeptide of claim 1 which comprises the amino acid sequence TERRRQQLDKDGDGTIDEREIKIHFQNKRAKIK (SEQ ID NO:2), or a [catalytically active] portion thereof which binds the nucleic acid sequence and the metal.